

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/563,779  
Source: IFW  
Date Processed by STIC: 8/25/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/563,779

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/563,779

DATE: 08/25/2006

TIME: 11:42:54

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\08252006\J563779.Fa

3 <110> APPLICANT: Syngenta Limited  
 5 <120> TITLE OF INVENTION: A method of selectively producing male or female sterile plants  
 7 <130> FILE REFERENCE: PPD70629  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/563,779  
 C--> 9 <141> CURRENT FILING DATE: 2006-01-06  
 E--> 9 <160> NUMBER OF SEQ ID NOS: (11) 7 ← see below  
 11 <170> SOFTWARE: PatentIn version 3.1

see item 4 on Error  
 summary  
 sheet

## ERRORED SEQUENCES

Does Not Comply  
 Corrected Diskette Needed

197 <210> SEQ ID NO: 7 ← last sequence in submitted file  
 198 <211> LENGTH: 7  
 199 <212> TYPE: PRT  
 200 <213> ORGANISM: Artificial Sequence  
 202 <220> FEATURE:  
 203 <223> OTHER INFORMATION (Motif) insufficient explanation - give source of genetic material  
 205 <400> SEQUENCE: 7 (same error in sequence 6)  
 207 Gly Gly Thr Tyr Gly Val Gly  
 208 1 5  
 E--> 216 - 3 - delete  
 (see item 11 on Error summary sheet)

## VERIFICATION SUMMARY

DATE: 08/25/2006

PATENT APPLICATION: US/10/563,779

TIME: 11:42:55

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\08252006\J563779.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:60  
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:60  
L:216 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:9 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (11) Counted (7)



PAGE: 1 VERIFICATION SUMMARY REPORT DATE:  
03/09/2007 PATENT APPLICATION TIME:  
09:41:35

INPUT SEQ: T:\Legal\IP\1PATENT\70269US Method  
of Producing Sterile Plants\70629 ST25.txt

GENERAL INFORMATION SECTION

3,<110> Syngenta Limited  
5,<120> A method of selectively producing male or female  
sterile plants  
7,<130> PPD70629  
9,<140> US/10/563,799  
10,<141> 2006-01-06  
12,<150> PCT/GB04/002447  
13,<151> 2004-06-09  
15,<150> GB 0316040.5  
16,<151> 2003-07-08  
18,<150> GB 0401839.6  
19,<151> 2004-01-28  
21,<160> 7  
23,<170> PatentIn version 3.3

ERRORED LINES SECTION

W--> 134 tccccatgca agcgatgcac gnnngactcg tccgaccccg cttctcccgc  
ctacatcatt 60  
W--> 136 ccccgaccag gtggcgaagt catctgcggc gggacgnnng gcgtgggaga  
ctgggacttg 120  
W--> 179 caagtcccag tctcccacgc cnnncgtccc gccgcagatg acttcgccac  
ctgggtcgggg 60  
W--> 181 aatgatgtag gcgggagaag cggggtcgga cgagtcnnnc gtgcatcgct  
tgcattgggga 120

STATISTICS SUMMARY

Application Serial Number: US/10/563,799  
Alpha or Numeric or Xml: Numeric  
Application Class:  
Application File Date: 2006-01-06  
Art Unit:  
Software Application: PatentIN3.3  
Total Number of Sequences: 7  
Total Nucleotides: 1408  
Total Amino Acids: 14  
Number of Errors: 0  
Number of Warnings: 4  
Number of Corrections: 0

PAGE: 1  
03/09/2007

ERROR LISTING  
PATENT APPLICATION

DATE:  
TIME:

09:41:35

INPUT SEQ: T:\Legal\IP\1PATENT\70269US Method  
of Producing Sterile Plants\70629 ST25.txt

L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:60  
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:60